

Sequence listing

<110> Sagami Chemical Research Center

5 <120> Human Proteins Having Transmembrane Domains and DNAs Encoding these Proteins

<130> 661099

10 <140>

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<150> JP 10-119395

<151> 1998-04-28

15

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<170> Windows 95 (Word 98)

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<210> 1

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<212> PRT

<213> Homo sapiens

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1

5

10

15

Gln Met Leu His Leu Val Phe Ile Leu Pro Ser Leu Met Leu Leu Ile

30

20

25

30

Pro His Ile Leu Leu Glu Asn Phe Ala Ala Ala Ile Pro Gly His Arg

35

40

45

Cys Trp Val His Met Leu Asp Asn Asn Thr Gly Ser Gly Asn Glu Thr

50

55

60

35

Gly Ile Leu Ser Glu Asp Ala Leu Leu Arg Ile Ser Ile Pro Leu Asp

09674235-031901

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	Thr	Glu	Pro	Cys	Val	Asp	Gly	Trp	Val	Tyr	Asp	Gln	Ser	Tyr	Phe	Pro
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	Ser	Thr	Ile	Val	Thr	Lys	Trp	Asp	Leu	Val	Cys	Asp	Tyr	Gln	Ser	Leu
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	145					150					155					160
	Ile	Ile	Gly	Gly	His	Val	Ser	Asp	Arg	Trp	Leu	Val	Glu	Ser	Ala	Arg
					165					170						175
	Trp	Leu	Ile	Ile	Thr	Asn	Lys	Leu	Asp	Glu	Gly	Leu	Lys	Ala	Leu	Arg
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	Lys	Val	Ala	Arg	Thr	Asn	Gly	Ile	Lys	Asn	Ala	Glu	Glu	Thr	Leu	Asn
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	Ile	Glu	Val	Val	Arg	Ser	Thr	Met	Gln	Glu	Glu	Leu	Asp	Ala	Ala	Gln
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20	Thr	Lys	Thr	Thr	Val	Cys	Asp	Leu	Phe	Arg	Asn	Pro	Ser	Met	Arg	Lys
	225					230					235					240
	Arg	Ile	Cys	Ile	Leu	Val	Phe	Leu	Arg	Lys	Lys	Ile	Ser	Arg	Lys	Arg
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30 <213> Homo sapiens

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 His Asp Leu Ile Phe Trp Arg Asp Val Lys Lys Thr Gly Phe Val Phe
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 Gly Thr Thr Leu Ile Met Leu Leu Ser Leu Ala Ala Phe Ser Val Ile
 65 70 75 80
 Ser Val Val Ser Tyr Leu Ile Leu Ala Leu Leu Ser Val Thr Ile Ser
 85 90 95
 10 Phe Arg Ile Tyr Lys Ser Val Ile Gln Ala Val Gln Lys Ser Glu Glu
 100 105 110
 Gly His Pro Phe Lys Ala Tyr Leu Asp Val Asp Ile Thr Leu Ser Ser
 115 120 125
 Glu Ala Phe His Asn Tyr Met Asn Ala Ala Met Val His Ile Asn Arg
 15 130 135 140
 Ala Leu Lys Leu Ile Ile Arg Leu Phe Leu Val Glu Asp Leu Val Asp
 145 150 155 160
 Ser Leu Lys Leu Ala Val Phe Met Trp Leu Met Thr Tyr Val Gly Ala
 165 170 175
 20 Val Phe Asn Gly Ile Thr Leu Leu Ile Leu Ala Glu Leu Leu Ile Phe
 180 185 190
 Ser Val Pro Ile Val Tyr Glu Lys Tyr Lys Thr Gln Ile Asp His Tyr
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 Val Gly Ile Ala Arg Asp Gln Thr Lys Ser Ile Val Glu Lys Ile Gln
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 Ala Lys Leu Pro Gly Ile Ala Lys Lys Lys Ala Glu
 225 230 235

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 <213> Homo sapiens

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09674235.031901

4.

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 Tyr Val Ser Ile Leu Leu Gln Ser Asp Lys Lys Leu Thr Gln Glu Gln
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 Val Ser Asp Ser Gln Val Leu Ile Arg Ser Arg Val Leu Arg Glu Asn
 50 55 60
 Gly Lys Tyr Ile Pro Lys Gln Ser Phe Leu Thr Arg Lys Tyr Tyr Phe
 65 70 75 80
 10 Asn Asn Pro Glu Asp Gly Phe Phe Lys Lys Thr Lys Arg Lys Val Val
 85 90 95
 Pro Pro Ser Pro Met Thr Asp Pro Thr Met Leu Thr Asp Met Met Lys
 100 105 110
 Gly Asn Val Thr Asn Val Leu Pro Met Ile Leu Ile Gly Gly Trp Ile
 15 115 120 125
 Asn Met Thr Phe Ser Gly Phe Val Thr Thr Lys Val Pro Phe Pro Leu
 130 135 140
 Thr Leu Arg Phe Lys Pro Met Leu Gln Gln Gly Ile Glu Leu Leu Thr
 145 150 155 160
 20 Leu Asp Ala Ser Trp Val Ser Ser Ala Ser Trp Tyr Phe Leu Asn Val
 165 170 175
 Phe Gly Leu Arg Ser Ile Tyr Ser Leu Ile Leu Gly Gln Asp Asn Ala
 180 185 190
 Ala Asp Gln Ser Arg Met Met Gln Glu Gln Met Thr Gly Ala Ala Met
 25 195 200 205
 Ala Met Pro Ala Asp Thr Asn Lys Ala Phe Lys Thr Glu Trp Glu Ala
 210 215 220
 Leu Glu Leu Thr Asp His Gln Trp Ala Leu Asp Asp Val Glu Glu Glu
 225 230 235 240
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 Gln Thr Ser Ile Phe
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Arg Met Lys Leu Leu Leu Gly Ile Ala Leu Leu Ala Tyr Val Ala Ser

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35 40 45

Gln Glu Asn Gly Glu Leu Lys Ile Glu Ser Lys Ile Glu Glu Met Val

50 55 60

Glu Pro Leu Arg Glu Lys Ile Arg Asp Leu Glu Lys Ser Phe Thr Gln

15 65 70 75 80

Lys Tyr Pro Pro Val Lys Phe Leu Ser Glu Lys Asp Arg Lys Arg Ile

85 90 95

Leu Ile Thr Gly Gly Ala Gly Phe Val Gly Ser His Leu Thr Asp Lys

100 105 110

20 Leu Met Met Asp Gly His Glu Val Thr Val Val Asp Asn Phe Phe Thr

115 120 125

Gly Arg Lys Arg Asn Val Glu His Trp Ile Gly His Glu Asn Phe Glu

130 135 140

Leu Ile Asn His Asp Val Val Glu Pro Leu Tyr Ile Glu Gly Val Glu

25 145 150 155 160

Val Arg Val Ala Arg Ile Phe Asn Thr Phe Gly Pro Arg Met His Met

165 170 175

Asn Asp Gly Arg Val Val Ser Asn Phe Ile Leu Gln Ala Leu Gln Gly

180 185 190

30 Glu Pro Leu Thr Val Tyr Gly Ser Gly Ser Gln Thr Arg Ala Phe Gln

195 200 205

Tyr Val Ser Asp Leu Val Asn Gly Leu Val Ala Leu Met Asn Ser Asn

210 215 220

Val Ser Ser Pro Val Asn Leu Gly Asn Pro Glu Glu His Thr Ile Leu

35 225 230 235 240

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[illegible]

Leu Phe Ala Thr Gln Asp Pro Gln Ile Glu Lys Thr Phe Glu Val Asn
 130 135 140
 Val Leu Ala His Phe Trp Thr Thr Lys Ala Phe Leu Pro Ala Met Thr
 145 150 155 160
 5 Lys Asn Asn His Gly His Ile Val Thr Val Ala Ser Ala Ala Gly His
 165 170 175
 Val Ser Val Pro Phe Leu Leu Ala Tyr Cys Ser Ser Lys Phe Ala Ala
 180 185 190
 Val Gly Phe His Lys Thr Leu Thr Asp Glu Leu Ala Ala Leu Gln Ile
 10 195 200 205
 Thr Gly Val Lys Thr Thr Cys Leu Cys Pro Asn Phe Val Asn Thr Gly
 210 215 220
 Phe Ile Lys Asn Pro Ser Thr Ser Leu Gly Pro Thr Leu Glu Pro Glu
 225 230 235 240
 15 Glu Val Val Asn Arg Leu Met His Gly Ile Leu Thr Glu Gln Lys Met
 245 250 255
 Ile Phe Ile Pro Ser Ser Ile Ala Phe Leu Thr Thr Leu Glu Arg Ile
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 20 275 280 285
 Phe Asp Ala Val Ile Gly Tyr Lys Met Lys Ala Gln
 290 295 300

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 Thr Ala Trp Ala Arg Arg Ser Gln Asp Leu His Cys Gly Ala Cys Arg
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 Ala Leu Val Asp Glu Leu Glu Trp Glu Ile Ala Gln Val Asp Pro Lys
 35 35 40 45

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Lys Thr Ile Gln Met Gly Ser Phe Arg Ile Asn Pro Asp Gly Ser Gln
 50 55 60
 Ser Val Val Glu Val Pro Tyr Ala Arg Ser Glu Ala His Leu Thr Glu
 65 70 75 80
 5 Leu Leu Glu Glu Ile Cys Asp Arg Met Lys Glu Tyr Gly Glu Gln Ile
 85 90 95
 Asp Pro Ser Thr His Arg Lys Asn Tyr Val Arg Val Val Gly Arg Asn
 100 105 110
 Gly Glu Ser Ser Glu Leu Asp Leu Gln Gly Ile Arg Ile Asp Ser Asp
 10 115 120 125
 Ile Ser Gly Thr Leu Lys Phe Ala Cys Glu Ser Ile Val Glu Glu Tyr
 130 135 140
 Glu Asp Glu Leu Ile Glu Phe Phe Ser Arg Glu Ala Asp Asn Val Lys
 145 150 155 160
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 165 170 175
 Ile Ser His Asp Glu Leu
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 35 40 45
 Trp Leu Phe Ile Leu Phe Asp Val Val Val Phe Leu Phe Val Tyr Phe
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 Leu Pro
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5 <213> Homo sapiens

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 35 40 45
 Leu Leu Leu Val Ala Lys Met Ser Val Gly His Leu Arg Leu Leu Ser
 15 50 55 60
 His Asp Gln Val Ala Met Pro Tyr Gln Trp Glu Tyr Pro Tyr Leu Leu
 65 70 75 80
 Ser Ile Leu Pro Ser Leu Leu Gly Leu Leu Ser Phe Pro Arg Asn Asn
 85 90 95
 20 Ile Ser Tyr Leu Val Leu Ser Met Ile Ser Met Gly Leu Phe Ser Ile
 100 105 110
 Ala Pro Leu Ile Tyr Gly Ser Met Glu Met Phe Pro Ala Ala Gln Gln
 115 120 125
 Leu Tyr Arg His Gly Lys Ala Tyr Arg Phe Leu Phe Gly Phe Ser Ala
 25 130 135 140
 Val Ser Ile Met Tyr Leu Val Leu Val Leu Ala Val Gln Val His Ala
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 Trp Gln Leu Tyr Tyr Ser Lys Lys Leu Leu Asp Ser Trp Phe Thr Ser
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 30 Thr Gln Glu Lys Lys His Lys
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 35 40 45
 10 Ile Cys Val Leu Arg Arg Pro Gly Ala Asn His Glu Gly Ser Ala Ser
 50 55 60
 Arg Gln Lys Ala Leu Ser Leu Val Ser Cys Phe Ala Gly Gly Val Phe
 65 70 75 80
 Leu Ala Thr Cys Leu Leu Asp Leu Leu Pro Asp Tyr Leu Ala Ala Ile
 15 85 90 95
 Asp Glu Ala Leu Ala Ala Leu His Val Thr Leu Gln Phe Pro Leu Gln
 100 105 110
 Glu Phe Ile Leu Ala Met Gly Phe Phe Leu Val Leu Val Met Glu Gln
 115 120 125
 20 Ile Thr Leu Ala Tyr Lys Glu Gln Ser Gly Pro Ser Pro Leu Glu Glu
 130 135 140
 Thr Arg Ala Leu Leu Gly Thr Val Asn Gly Gly Pro Gln His Trp His
 145 150 155 160
 Asp Gly Pro Gly Val Pro Gln Ala Ser Gly Ala Pro Ala Thr Pro Ser
 25 165 170 175
 Ala Leu Arg Ala Cys Val Leu Val Phe Ser Leu Ala Leu His Ser Val
 180 185 190
 Phe Glu Gly Leu Ala Val Gly Leu Gln Arg Asp Arg Ala Arg Ala Met
 195 200 205
 30 Glu Leu Cys Leu Ala Leu Leu Leu His Lys Gly Ile Leu Ala Val Ser
 210 215 220
 Leu Ser Leu Arg Leu Leu Gln Ser His Leu Arg Ala Gln Val Val Ala
 225 230 235 240
 Gly Cys Gly Ile Leu Phe Ser Cys Met Thr Pro Leu Gly Ile Gly Leu
 35 245 250 255

09674235.031904
FOUO" 55247950



Gly	Ala	Ala	Leu	Ala	Glu	Ser	Ala	Gly	Pro	Leu	His	Gln	Leu	Ala	Gln		
260						265						270					
Ser	Val	Leu	Glu	Gly	Met	Ala	Ala	Gly	Thr	Phe	Leu	Tyr	Ile	Thr	Phe		
275						280						285					
Leu	Glu	Ile	Leu	Pro	Gln	Glu	Leu	Ala	Ser	Ser	Glu	Gln	Arg	Ile	Leu		
290						295						300					
Lys	Val	Ile	Leu	Leu	Leu	Ala	Gly	Phe	Ala	Leu	Leu	Thr	Gly	Leu	Leu		
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Phe		Ile		Gln		Ile											

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accaataaac	tagatgaggg	cttaaaggca	cttagaaaag	ttgcacgcac	aaatggaata	600
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gatgcagcac	agacaaaaac	tactgtgtgt	gacttggttc	gcaaccccag	tatgcgtaaa	720
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	atcacccttc	taattcttgc	tgaactgtc	attttcagt	tcccgattgt	ctatgagaag	600
	tacaagaccc	agattgatca	ctatgttggc	atcgcccag	atcagaccaa	gtcaattgtt	660
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	gacaagaagc	tcaccagga	acaagtatct	gacagtcaag	tcctaattcg	aagcagagtc	180
25	ctcagggaaa	atggaaaata	cattcccaaa	cagtctttct	tgacacgaaa	atattatttc	240
	aacaaccag	aggatggatt	tttcaaaaaa	actaaacgga	aggtagtgcc	accttctcct	300
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	atgattctta	ttggtggatg	gatcaacatg	acattctcag	gctttgtcac	aaccaaggtc	420
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<212> DNA

5 <213> Homo sapiens

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 gaagagatgg ttgaaccact aagagagaaa atcagagatt tagaaaaaag ctttaccag 240
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 15 gagaacttcg agttgattaa ccacgacgtg gtggagcccc tctacatcga gggcgtggaa 480
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 ggggtgggagc ccgtggtccc gctggaggaa ggtttaaaca aagcaattca ctacttccgt 900
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 aagaaaggac ggactcgcca cagc 984

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 gctggtgtag tctatacatc agatttggtt gctacacaag atcctcagat tgaaaagact 420
 tttgaagtta atgtacttgc acatttctgg actacaaagg catttcttcc tgcaatgacg 480
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 ttcttactgg cttactgttc aagcaagttt gctgctgttg gatttcataa aactttgaca 600
 gatgaactgg ctgccttaca aataactgga gtcaaaacaa catgtctgtg tcctaatttc 660
 gtaaactg gcttcatcaa aaatccaagt acaagtttg gaccactct ggaacctgag 720
 gaagtggtaa acaggctgat gcatgggatt ctgactgagc agaagatgat ttttattcca 780
 10 tcttctatag cttttttaac aacattggaa aggatccttc ctgagcggtt cctggcagtt 840
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 gaaattgccc aggtggaccc caagaagacc attcagatgg gatctttccg gatcaatcca 180
 gatggcagcc agtcagtggg ggaggtgcct tatgcccgct cagaggccca cctcacagag 240
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 catcgcaaga actacgtacg tgtagtgggc cggaatggag aatccagtga actggacct 360
 25 caaggcatcc gaatcgactc agatattagc ggcacctca agtttgctg tgagagcatt 420
 gtggaggaat acgaggatga actcattgaa ttcttttccc gagaggctga caatgttaaa 480
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 aaacactcct actggttgga cctctggcct ttcactcttt tcgatgtggg ggtgtttctc 180
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<210> 17

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<212> DNA

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 atctacgtac atctggatcat atggtgctg ctggttgcta agatgagcgt gggacacctg 180
 15 aggetcttgt cacatgatca ggtggccatg ccctatcagt gggaataccc gtatttgctg 240
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	ctt aga aaa gtt gca cgc aca aat gga ata aag aat gct gaa gaa acc	804
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	195 200 205	
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 35 40 45
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 50 55 60
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 35 Ala Asp Thr Glu Pro Cys Val Asp Gly Trp Val Tyr Asp Gln Ser Tyr

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19.

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	Gly Lys Tyr Ile Pro Lys Gln Ser Phe Leu Thr Arg Lys Tyr Tyr Phe	
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 Phe Gly Leu Arg Ser Ile Tyr Ser Leu Ile Leu Gly Gln Asp Asn Ala
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	Lys Tyr Pro Pro Val Lys Phe Leu Ser Glu Lys Asp Arg Lys Arg Ile	
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	225	230	235	240
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	Glu Phe Ala Gln Leu Ile Lys Asn Leu Val Gly Ser Gly Ser Glu Ile			
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	cag ttt ctc tcc gaa gcc cag gat gac cca cag aaa aga aaa cca gac			874
	Gln Phe Leu Ser Glu Ala Gln Asp Asp Pro Gln Lys Arg Lys Pro Asp			
	260	265	270	
	atc aaa aaa gca aag ctg atg ctg ggg tgg gag ccc gtg gtc ccg ctg			922
15	Ile Lys Lys Ala Lys Leu Met Leu Gly Trp Glu Pro Val Val Pro Leu			
	275	280	285	
	gag gaa ggt tta aac aaa gca att cac tac ttc cgt aaa gaa ctc gag			970
	Glu Glu Gly Leu Asn Lys Ala Ile His Tyr Phe Arg Lys Glu Leu Glu			
	290	295	300	
20	tac cag gca aat aat cag tac atc ccc aaa cca aag cct gcc aga ata			1018
	Tyr Gln Ala Asn Asn Gln Tyr Ile Pro Lys Pro Lys Pro Ala Arg Ile			
	305	310	315	320
	aag aaa gga cgg act cgc cac agc tgaactcctc acttttagga cacaagac			1070
	Lys Lys Gly Arg Thr Arg His Ser			
25	325			
	taccattgta cacttgatgg gatgtatttt tggctttttt ttgttgctgt ttaaagaaag			1130
	actttaacag gtgtcatgaa gaacaaactg gaatttcatt ctgaagcttg ctttaatgaa			1190
	atggatgtgc ctaaaagctc cccataaaaa actgcagatt ttgccttgca ctttttgaat			1250
	ctctcttttt atgtaaaata gcgtagatgc atctctgcgt attttcaagt ttttttatct			1310
30	tgctgtgaga gcatatgttg tgactgtcgt tgacagtttt atttactggg ttctttgtga			1370
	agctgaaaag gaacattaag cgggacaaaa aatgccgatt ttatttataa aagtgggtac			1430
	ttaataaatg agtcgttata ctatgcataa agaaaaatcc tagcagtatt gtcaggtggt			1490
	ggtgcgccgg cattgatttt agggcagata aaagaattct gtgtgagagc tttatgtttc			1550
	tcttttaatt cagagttttt ccaaggtcta cttttgagtt gcaaacttga ctttgaaata			1610
35	ttcctgttgg tcatgatcaa ggatatttga aatcactact gtgttttgct gcgtatctgg			1670

ggcgggggca ggttgggggg cacaaagtta acatattcctt ggtaaacat ggtaaatat 1730
gctattttaa taaaatattg aaactcacc 1759

<210> 26

5 <211> 328

<212> PRT

<213> Homo sapiens

<400> 26

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Arg Met Lys Leu Leu Leu Gly Ile Ala Leu Leu Ala Tyr Val Ala Ser
20 25 30
Val Trp Gly Asn Phe Val Asn Met Ser Phe Leu Leu Asn Arg Ser Ile
15 35 40 45
Gln Glu Asn Gly Glu Leu Lys Ile Glu Ser Lys Ile Glu Glu Met Val
50 55 60
Glu Pro Leu Arg Glu Lys Ile Arg Asp Leu Glu Lys Ser Phe Thr Gln
65 70 75 80
20 Lys Tyr Pro Pro Val Lys Phe Leu Ser Glu Lys Asp Arg Lys Arg Ile
85 90 95
Leu Ile Thr Gly Gly Ala Gly Phe Val Gly Ser His Leu Thr Asp Lys
100 105 110
Leu Met Met Asp Gly His Glu Val Thr Val Val Asp Asn Phe Phe Thr
25 115 120 125
Gly Arg Lys Arg Asn Val Glu His Trp Ile Gly His Glu Asn Phe Glu
130 135 140
Leu Ile Asn His Asp Val Val Glu Pro Leu Tyr Ile Glu Gly Val Glu
145 150 155 160
30 Val Arg Val Ala Arg Ile Phe Asn Thr Phe Gly Pro Arg Met His Met
165 170 175
Asn Asp Gly Arg Val Val Ser Asn Phe Ile Leu Gln Ala Leu Gln Gly
180 185 190
Glu Pro Leu Thr Val Tyr Gly Ser Gly Ser Gln Thr Arg Ala Phe Gln
35 195 200 205

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FOOTED SECH/960

Tyr Val Ser Asp Leu Val Asn Gly Leu Val Ala Leu Met Asn Ser Asn
 210 215 220
 Val Ser Ser Pro Val Asn Leu Gly Asn Pro Glu Glu His Thr Ile Leu
 225 230 235 240
 5 Glu Phe Ala Gln Leu Ile Lys Asn Leu Val Gly Ser Gly Ser Glu Ile
 245 250 255
 Gln Phe Leu Ser Glu Ala Gln Asp Asp Pro Gln Lys Arg Lys Pro Asp
 260 265 270
 Ile Lys Lys Ala Lys Leu Met Leu Gly Trp Glu Pro Val Val Pro Leu
 10 275 280 285
 Glu Glu Gly Leu Asn Lys Ala Ile His Tyr Phe Arg Lys Glu Leu Glu
 290 295 300
 Tyr Gln Ala Asn Asn Gln Tyr Ile Pro Lys Pro Lys Pro Ala Arg Ile
 305 310 315 320
 15 Lys Lys Gly Arg Thr Arg His Ser
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 <210> 27
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 20 <212> DNA
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 <400> 27
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 ccacaaaagg g atg aaa ttt ctt ctg gac atc ctc ctg ctt ctc ccg tta 170
 Met Lys Phe Leu Leu Asp Ile Leu Leu Leu Leu Pro Leu
 1 5 10
 ctg atc gtc tgc tcc cta gag tcc ttc gtg aag ctt ttt att cct aag 218
 30 Leu Ile Val Cys Ser Leu Glu Ser Phe Val Lys Leu Phe Ile Pro Lys
 15 20 25
 agg aga aaa tca gtc acc ggc gaa atc gtg ctg att aca gga gct ggg 266
 Arg Arg Lys Ser Val Thr Gly Glu Ile Val Leu Ile Thr Gly Ala Gly
 30 35 40 45
 35 cat gga att ggg aga ctg act gcc tat gaa ttt gct aaa ctt aaa agc 314

09674235.031901
 T067E0" SE274960

	His Gly Ile Gly Arg Leu Thr Ala Tyr Glu Phe Ala Lys Leu Lys Ser	
	50	55 60
	aag ctg gtt ctc tgg gat ata aat aag cat gga ctg gag gaa aca gct	362
	Lys Leu Val Leu Trp Asp Ile Asn Lys His Gly Leu Glu Glu Thr Ala	
5	65	70 75
	gcc aaa tgc aag gga ctg ggt gcc aag gtt cat acc ttt gtg gta gac	410
	Ala Lys Cys Lys Gly Leu Gly Ala Lys Val His Thr Phe Val Val Asp	
	80	85 90
	tgc agc aac cga gaa gat att tac agc tct gca aag aag gtg aag gca	458
10	Cys Ser Asn Arg Glu Asp Ile Tyr Ser Ser Ala Lys Lys Val Lys Ala	
	95	100 105
	gaa att gga gat gtt agt att tta gta aat aat gct ggt gta gtc tat	506
	Glu Ile Gly Asp Val Ser Ile Leu Val Asn Asn Ala Gly Val Val Tyr	
	110	115 120 125
15	aca tca gat ttg ttt gct aca caa gat cct cag att gaa aag act ttt	554
	Thr Ser Asp Leu Phe Ala Thr Gln Asp Pro Gln Ile Glu Lys Thr Phe	
	130	135 140
	gaa gtt aat gta ctt gca cat ttc tgg act aca aag gca ttt ctt cct	602
	Glu Val Asn Val Leu Ala His Phe Trp Thr Thr Lys Ala Phe Leu Pro	
20	145	150 155
	gca atg acg aag aat aac cat ggc cat att gtc act gtg gct tcg gca	650
	Ala Met Thr Lys Asn Asn His Gly His Ile Val Thr Val Ala Ser Ala	
	160	165 170
	gct gga cat gtc tcg gtc ccc ttc tta ctg gct tac tgt tca agc aag	698
25	Ala Gly His Val Ser Val Pro Phe Leu Leu Ala Tyr Cys Ser Ser Lys	
	175	180 185
	ttt gct gct gtt gga ttt cat aaa act ttg aca gat gaa ctg gct gcc	746
	Phe Ala Ala Val Gly Phe His Lys Thr Leu Thr Asp Glu Leu Ala Ala	
	190	195 200 205
30	tta caa ata act gga gtc aaa aca aca tgt ctg tgt cct aat ttc gta	794
	Leu Gln Ile Thr Gly Val Lys Thr Thr Cys Leu Cys Pro Asn Phe Val	
	210	215 220
	aac act ggc ttc atc aaa aat cca agt aca agt ttg gga ccc act ctg	842
	Asn Thr Gly Phe Ile Lys Asn Pro Ser Thr Ser Leu Gly Pro Thr Leu	
35	225	230 235

	gaa cct gag gaa gtg gta aac agg ctg atg cat ggg att ctg act gag	890
	Glu Pro Glu Glu Val Val Asn Arg Leu Met His Gly Ile Leu Thr Glu	
	240 245 250	
	cag aag atg att ttt att cca tct tct ata gct ttt tta aca aca ttg	938
5	Gln Lys Met Ile Phe Ile Pro Ser Ser Ile Ala Phe Leu Thr Thr Leu	
	255 260 265	
	gaa agg atc ctt cct gag cgt ttc ctg gca gtt tta aaa cga aaa atc	986
	Glu Arg Ile Leu Pro Glu Arg Phe Leu Ala Val Leu Lys Arg Lys Ile	
	270 275 280 285	
10	agt gtt aag ttt gat gca gtt att gga tat aaa atg aaa gcg caa	1031
	Ser Val Lys Phe Asp Ala Val Ile Gly Tyr Lys Met Lys Ala Gln	
	290 295 300	
	taagcacct agttttctga aaactgattt accaggttta ggttgatgtc atctaatagt	1090
	gccagaattt taatgtttga acttctgttt tttctaatta tccccatttc ttcaatatca	1150
15	tttttgaggc ttggcagtc ttcatttact accacttggt ctttagccaa aagctgatta	1210
	catatgatat aaacagagaa ataccttag aggtgacttt aaggaaaatg aagaaaaaga	1270
	acaaaaatga ctttattaaa ataattcca agattatttg tggctcacct gaaggctttg	1330
	caaaatttgt accataaccg tttattttaac atatattttt atttttgatt gcacttaa	1390
	tttgtataat ttgtgtttct ttttctgttc tacataaaat cagaaacttc aagctctcta	1450
20	aataaaatga aggactatat ctagtgggtat ttcacaatga atatcatgaa ctctcaatgg	1510
	gtaggtttca tcctacccat tgccactctg tttcctgaga gatacctcac attccaatgc	1570
	caaacatttc tgcacaggga agctagaggt ggatacacgt gttgcaagta taaaagcatc	1630
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	cacactt	1697
25		
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30		
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	Met Lys Phe Leu Leu Asp Ile Leu Leu Leu Leu Pro Leu	
	1 5 10	
	Leu Ile Val Cys Ser Leu Glu Ser Phe Val Lys Leu Phe Ile Pro Lys	
35	15 20 25	

Figure 1 consists of 12 histograms arranged vertically, each representing a different value of n from 10 to 120 in increments of 10. The x-axis for all histograms is labeled 'x' and ranges from 0 to 120. The y-axis is labeled 'count' and ranges from 0 to 100. The histograms show that as n increases, the distribution of the number of non-zero elements in the vector x becomes increasingly concentrated around zero. For $n=10$, the distribution is broad and low, with a peak count of approximately 10. As n increases, the peak at zero grows, reaching a count of 100 for $n=120$, while the counts for other values of x decrease.

32.

Arg Arg Lys Ser Val Thr Gly Glu Ile Val Leu Ile Thr Gly Ala Gly
 30 35 40 45
 His Gly Ile Gly Arg Leu Thr Ala Tyr Glu Phe Ala Lys Leu Lys Ser
 50 55 60
 5 Lys Leu Val Leu Trp Asp Ile Asn Lys His Gly Leu Glu Glu Thr Ala
 65 70 75
 Ala Lys Cys Lys Gly Leu Gly Ala Lys Val His Thr Phe Val Val Asp
 80 85 90
 Cys Ser Asn Arg Glu Asp Ile Tyr Ser Ser Ala Lys Lys Val Lys Ala
 10 95 100 105
 Glu Ile Gly Asp Val Ser Ile Leu Val Asn Asn Ala Gly Val Val Tyr
 110 115 120 125
 Thr Ser Asp Leu Phe Ala Thr Gln Asp Pro Gln Ile Glu Lys Thr Phe
 130 135 140
 15 Glu Val Asn Val Leu Ala His Phe Trp Thr Thr Lys Ala Phe Leu Pro
 145 150 155
 Ala Met Thr Lys Asn Asn His Gly His Ile Val Thr Val Ala Ser Ala
 160 165 170
 Ala Gly His Val Ser Val Pro Phe Leu Leu Ala Tyr Cys Ser Ser Lys
 20 175 180 185
 Phe Ala Ala Val Gly Phe His Lys Thr Leu Thr Asp Glu Leu Ala Ala
 190 195 200 205
 Leu Gln Ile Thr Gly Val Lys Thr Thr Cys Leu Cys Pro Asn Phe Val
 210 215 220
 25 Asn Thr Gly Phe Ile Lys Asn Pro Ser Thr Ser Leu Gly Pro Thr Leu
 225 230 235
 Glu Pro Glu Glu Val Val Asn Arg Leu Met His Gly Ile Leu Thr Glu
 240 245 250
 Gln Lys Met Ile Phe Ile Pro Ser Ser Ile Ala Phe Leu Thr Thr Leu
 30 255 260 265
 Glu Arg Ile Leu Pro Glu Arg Phe Leu Ala Val Leu Lys Arg Lys Ile
 270 275 280 285
 Ser Val Lys Phe Asp Ala Val Ile Gly Tyr Lys Met Lys Ala Gln
 290 295 300
 35

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 T062E0-5247960

<210> 29

<211> 814

<212> DNA

<213> Homo sapiens

5

<400> 29

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tggagcgacc ccattacgt aaag atg aaa ggc tgg ggt tgg ctg gcc ctg 171
Met Lys Gly Trp Gly Trp Leu Ala Leu
1 5
ctt ctg ggg gcc ctg ctg gga acc gcc tgg gct cgg agg agc cag gat 219
Leu Leu Gly Ala Leu Leu Gly Thr Ala Trp Ala Arg Arg Ser Gln Asp
10 15 20 25
ctc cac tgt gga gca tgc agg gct ctg gtg gat gaa cta gaa tgg gaa 267
Leu His Cys Gly Ala Cys Arg Ala Leu Val Asp Glu Leu Glu Trp Glu
30 35 40
att gcc cag gtg gac ccc aag aag acc att cag atg gga tct ttc cgg 315
Ile Ala Gln Val Asp Pro Lys Lys Thr Ile Gln Met Gly Ser Phe Arg
45 50 55
atc aat cca gat ggc agc cag tca gtg gtg gag gtg cct tat gcc cgc 363
Ile Asn Pro Asp Gly Ser Gln Ser Val Val Glu Val Pro Tyr Ala Arg
60 65 70
tca gag gcc cac ctc aca gag ctg ctg gag gag ata tgt gac cgg atg 411
Ser Glu Ala His Leu Thr Glu Leu Leu Glu Glu Ile Cys Asp Arg Met
75 80 85
aag gag tat ggg gaa cag att gat cct tcc acc cat cgc aag aac tac 459
Lys Glu Tyr Gly Glu Gln Ile Asp Pro Ser Thr His Arg Lys Asn Tyr
90 95 100 105
gta cgt gta gtg ggc cgg aat gga gaa tcc agt gaa ctg gac cta caa 507
Val Arg Val Val Gly Arg Asn Gly Glu Ser Ser Glu Leu Asp Leu Gln
110 115 120
ggc atc cga atc gac tca gat att agc ggc acc ctc aag ttt gcg tgt 555
Gly Ile Arg Ile Asp Ser Asp Ile Ser Gly Thr Leu Lys Phe Ala Cys
125 130 135

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gag agc att gtg gag gaa tac gag gat gaa ctc att gaa ttc ttt tcc 603
 Glu Ser Ile Val Glu Glu Tyr Glu Asp Glu Leu Ile Glu Phe Phe Ser
 140 145 150
 cga gag gct gac aat gtt aaa gac aaa ctt tgc agt aag cga aca gat 651
 5 Arg Glu Ala Asp Asn Val Lys Asp Lys Leu Cys Ser Lys Arg Thr Asp
 155 160 165
 ctt tgt gac cat gcc ctg cac ata tcg cat gat gag cta tgaaccactg 700
 Leu Cys Asp His Ala Leu His Ile Ser His Asp Glu Leu
 170 175 180
 10 gagcagccca cactggcttg atggatcacc cccaggaggg gaaaatggtg gcaatgcctt 760
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 <211> 182
 15 <212> PRT
 <213> Homo sapiens

 <400> 30

 Met Lys Gly Trp Gly Trp Leu Ala Leu
 20 1 5
 Leu Leu Gly Ala Leu Leu Gly Thr Ala Trp Ala Arg Arg Ser Gln Asp
 10 15 20 25
 Leu His Cys Gly Ala Cys Arg Ala Leu Val Asp Glu Leu Glu Trp Glu
 30 35 40
 25 Ile Ala Gln Val Asp Pro Lys Lys Thr Ile Gln Met Gly Ser Phe Arg
 45 50 55
 Ile Asn Pro Asp Gly Ser Gln Ser Val Val Glu Val Pro Tyr Ala Arg
 60 65 70
 Ser Glu Ala His Leu Thr Glu Leu Leu Glu Glu Ile Cys Asp Arg Met
 30 75 80 85
 Lys Glu Tyr Gly Glu Gln Ile Asp Pro Ser Thr His Arg Lys Asn Tyr
 90 95 100 105
 Val Arg Val Val Gly Arg Asn Gly Glu Ser Ser Glu Leu Asp Leu Gln
 110 115 120
 35 Gly Ile Arg Ile Asp Ser Asp Ile Ser Gly Thr Leu Lys Phe Ala Cys

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35.

125 130 135
 Glu Ser Ile Val Glu Glu Tyr Glu Asp Glu Leu Ile Glu Phe Phe Ser
 140 145 150
 Arg Glu Ala Asp Asn Val Lys Asp Lys Leu Cys Ser Lys Arg Thr Asp
 5 155 160 165
 Leu Cys Asp His Ala Leu His Ile Ser His Asp Glu Leu
 170 175 180

 <210> 31
 10 <211> 511
 <212> DNA
 <213> Homo sapiens

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 Met Glu Val Asp Ala Pro Gly Val Asp Gly
 1 5 10
 CGA GAT GGT CTC CGG GAG CGG CGA GGC TTT AGC GAG GGA GGG AGG CAG 100
 Arg Asp Gly Leu Arg Glu Arg Arg Gly Phe Ser Glu Gly Gly Arg Gln
 20 15 20 25
 aac ttc gat gtg agg cct cag tct ggg gca aat ggg ctt ccc aaa cac 148
 Asn Phe Asp Val Arg Pro Gln Ser Gly Ala Asn Gly Leu Pro Lys His
 30 35 40
 tcc tac tgg ttg gac ctc tgg ctt ttc atc ctt ttc gat gtg gtg gtg 196
 25 Ser Tyr Trp Leu Asp Leu Trp Leu Phe Ile Leu Phe Asp Val Val Val
 45 50 55
 ttt ctc ttt gtg tat ttt ttg cca tgacttggtc gctgatatct aaattaagaa 250
 Phe Leu Phe Val Tyr Phe Leu Pro
 60 65
 30 gttggttctt gagtgaattc tgaaaatggc tacaaacttc ttgaataaag aagacaggac 310
 tctcaataga agaatttcac atctccaagg gacccttcct ttcattttac actttgttac 370
 taatttgcag aactctatta attgggtagg atttcaccca ttcctagcta agttcttaaa 430
 attaaaccct ttggttcgtg tttaaaaact ttcaaacatc tgatggcttt acaggggctg 490
 aatataaaaag catttgtact t 511

35

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<210> 32

<211> 66

<212> PRT

<213> Homo sapiens

5

<400> 32

Met Glu Val Asp Ala Pro Gly Val Asp Gly
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15 20 25
Asn Phe Asp Val Arg Pro Gln Ser Gly Ala Asn Gly Leu Pro Lys His
30 35 40
Ser Tyr Trp Leu Asp Leu Trp Leu Phe Ile Leu Phe Asp Val Val Val
45 50 55
Phe Leu Phe Val Tyr Phe Leu Pro
60 65

<210> 33
<211> 1126
20 <212> DNA
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Met
1
gcg tct cga gca ggc ccg cga gcg gcc ggc acc gac ggc agc gac ttt 164
Ala Ser Arg Ala Gly Pro Arg Ala Ala Gly Thr Asp Gly Ser Asp Phe
5 10 15
cag cac cgg gag cgc gtc gcc atg cac tac cag atg agt gtg acc ctc 212
Gln His Arg Glu Arg Val Ala Met His Tyr Gln Met Ser Val Thr Leu
20 25 30
aag tat gaa atc aag aag ctg atc tac gta cat ctg gtc ata tgg ctg 260
35 Lys Tyr Glu Ile Lys Lys Leu Ile Tyr Val His Leu Val Ile Trp Leu

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	Leu Leu Val Ala Lys Met Ser Val Gly His Leu Arg Leu Leu Ser His			
	50	55	60	65
5	gat cag gtg gcc atg ccc tat cag tgg gaa tac ccg tat ttg ctg agc	356		
	Asp Gln Val Ala Met Pro Tyr Gln Trp Glu Tyr Pro Tyr Leu Leu Ser			
	70	75	80	
	att ttg ccc tct ctc ttg ggc ctt ctc tcc ttt ccc cgc aac aac att	404		
	Ile Leu Pro Ser Leu Leu Gly Leu Leu Ser Phe Pro Arg Asn Asn Ile			
10	85	90	95	
	agc tac ctg gtg ctc tcc atg atc agc atg gga ctc ttt tcc atc gct	452		
	Ser Tyr Leu Val Leu Ser Met Ile Ser Met Gly Leu Phe Ser Ile Ala			
	100	105	110	
	cca ctc att tat ggc agc atg gag atg ttc cct gct gca cag cag ctc	500		
15	Pro Leu Ile Tyr Gly Ser Met Glu Met Phe Pro Ala Ala Gln Gln Leu			
	115	120	125	
	tac cgc cat ggc aag gcc tac cgt ttc ctc ttt ggt ttt tct gcc gtt	548		
	Tyr Arg His Gly Lys Ala Tyr Arg Phe Leu Phe Gly Phe Ser Ala Val			
	130	135	140	145
20	tcc atc atg tac ctg gtg ttg gtg ttg gca gtg caa gtg cat gcc tgg	596		
	Ser Ile Met Tyr Leu Val Leu Val Leu Ala Val Gln Val His Ala Trp			
	150	155	160	
	cag ttg tac tac agc aag aag ctc cta gac tct tgg ttc acc agc aca	644		
	Gln Leu Tyr Tyr Ser Lys Lys Leu Leu Asp Ser Trp Phe Thr Ser Thr			
25	165	170	175	
	cag gag aag aag cat aaa tgaagcctct ttgggggtgaa gcctggacat cccatcga	700		
	Gln Glu Lys Lys His Lys			
	180			
	atgaaaggac actagtacag cggttccaaa atcccttctg gtgattttag cagctgtgat	760		
30	gttggtacct ggtgcagacc aggccaaagt tctggaaagc tccttttgcc atctgctgag	820		
	gtggcaaaac tataatttat tcttggttg ctagaactgg gtgaccgaca gctatgaaac	880		
	aaatttcagc tgtttgaagt tgaactttga ggtttttctt taagaatgag cttcgtcctt	940		
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	gaaataggga ataaatcaaa ttacttcatc tctaggtcac gggtcaggaa acatttgggc	1060		
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aagatg

1126

<210> 34

<211> 183

5 <212> PRT

<213> Homo sapiens

<400> 34

Met

10

1

Ala Ser Arg Ala Gly Pro Arg Ala Ala Gly Thr Asp Gly Ser Asp Phe

5

10

15

Gln His Arg Glu Arg Val Ala Met His Tyr Gln Met Ser Val Thr Leu

20

25

30

15

Lys Tyr Glu Ile Lys Lys Leu Ile Tyr Val His Leu Val Ile Trp Leu

35

40

45

Leu Leu Val Ala Lys Met Ser Val Gly His Leu Arg Leu Leu Ser His

50

55

60

65

Asp Gln Val Ala Met Pro Tyr Gln Trp Glu Tyr Pro Tyr Leu Leu Ser

20

70

75

80

Ile Leu Pro Ser Leu Leu Gly Leu Leu Ser Phe Pro Arg Asn Asn Ile

85

90

95

Ser Tyr Leu Val Leu Ser Met Ile Ser Met Gly Leu Phe Ser Ile Ala

100

105

110

25

Pro Leu Ile Tyr Gly Ser Met Glu Met Phe Pro Ala Ala Gln Gln Leu

115

120

125

Tyr Arg His Gly Lys Ala Tyr Arg Phe Leu Phe Gly Phe Ser Ala Val

130

135

140

145

Ser Ile Met Tyr Leu Val Leu Val Leu Ala Val Gln Val His Ala Trp

30

150

155

160

Gln Leu Tyr Tyr Ser Lys Lys Leu Leu Asp Ser Trp Phe Thr Ser Thr

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170

175

Gln Glu Lys Lys His Lys

180

35

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FOOTED" SECT 2960

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<211> 2015

<212> DNA

<213> Homo sapiens

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<400> 35

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	5 10 15	
	gct tca gag cct cca gtg cct gtg ggg ctg gag gtg aag ttg ggg gcc	152
	Ala Ser Glu Pro Pro Val Pro Val Gly Leu Glu Val Lys Leu Gly Ala	
15	20 25 30	
	ctg gtg ctg ctg ctg gtg ctc acc ctc ctc tgc agc ctg gtg ccc atc	200
	Leu Val Leu Leu Leu Val Leu Thr Leu Leu Cys Ser Leu Val Pro Ile	
	35 40 45	
	tgt gtg ctg cgc cgg cca gga gct aac cat gaa ggc tca gct tcc cgc	248
20	Cys Val Leu Arg Arg Pro Gly Ala Asn His Glu Gly Ser Ala Ser Arg	
	50 55 60 65	
	cag aaa gcc ctg agc cta gta agc tgt ttc gcg ggg ggc gtc ttt ttg	296
	Gln Lys Ala Leu Ser Leu Val Ser Cys Phe Ala Gly Gly Val Phe Leu	
	70 75 80	
25	gcc act tgt ctc ctg gac ctg ctg cct gac tac ctg gct gcc ata gat	344
	Ala Thr Cys Leu Leu Asp Leu Leu Pro Asp Tyr Leu Ala Ala Ile Asp	
	85 90 95	
	gag gcc ctg gca gcc ttg cac gtg acg ctc cag ttc cca ctg caa gag	392
	Glu Ala Leu Ala Ala Leu His Val Thr Leu Gln Phe Pro Leu Gln Glu	
30	100 105 110	
	ttc atc ctg gcc atg ggc ttc ttc ctg gtc ctg gtg atg gag cag atc	440
	Phe Ile Leu Ala Met Gly Phe Phe Leu Val Leu Val Met Glu Gln Ile	
	115 120 125	
	aca ctg gct tac aag gag cag tca ggg ccg tca cct ctg gag gaa aca	488
35	Thr Leu Ala Tyr Lys Glu Gln Ser Gly Pro Ser Pro Leu Glu Glu Thr	

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	130	135	140	145	
	agg gct ctg ctg gga aca gtg aat ggt ggg ccg cag cat tgg cat gat				536
	Arg Ala Leu Leu Gly Thr Val Asn Gly Gly Pro Gln His Trp His Asp				
		150	155	160	
5	ggg cca ggg gtc cca cag gcg agt gga gcc cca gca acc ccc tca gcc				584
	Gly Pro Gly Val Pro Gln Ala Ser Gly Ala Pro Ala Thr Pro Ser Ala				
		165	170	175	
	ttg cgt gcc tgt gta ctg gtg ttc tcc ctg gcc ctc cac tcc gtg ttc				632
	Leu Arg Ala Cys Val Leu Val Phe Ser Leu Ala Leu His Ser Val Phe				
10		180	185	190	
	gag ggg ctg gcg gta ggg ctg cag cga gac cgg gct cgg gcc atg gag				680
	Glu Gly Leu Ala Val Gly Leu Gln Arg Asp Arg Ala Arg Ala Met Glu				
		195	200	205	
	ctg tgc ctg gct ttg ctg ctc cac aag ggc atc ctg gct gtc agc ctg				728
15	Leu Cys Leu Ala Leu Leu Leu His Lys Gly Ile Leu Ala Val Ser Leu				
	210	215	220	225	
	tcc ctg cgg ctg ttg cag agc cac ctt agg gca cag gtg gtg gct ggc				776
	Ser Leu Arg Leu Leu Gln Ser His Leu Arg Ala Gln Val Val Ala Gly				
		230	235	240	
20	tgt ggg atc ctc ttc tca tgc atg aca cct cta ggc atc ggg ctg ggt				824
	Cys Gly Ile Leu Phe Ser Cys Met Thr Pro Leu Gly Ile Gly Leu Gly				
		245	250	255	
	gca gct ctg gca gag tcg gca gga cct ctg cac cag ctg gcc cag tct				872
	Ala Ala Leu Ala Glu Ser Ala Gly Pro Leu His Gln Leu Ala Gln Ser				
25		260	265	270	
	gtg cta gag ggc atg gca gct ggc acc ttt ctc tat atc acc ttt ctg				920
	Val Leu Glu Gly Met Ala Ala Gly Thr Phe Leu Tyr Ile Thr Phe Leu				
		275	280	285	
	gaa atc ctg ccc cag gag ctg gcc agt tct gag caa agg atc ctc aag				968
30	Glu Ile Leu Pro Gln Glu Leu Ala Ser Ser Glu Gln Arg Ile Leu Lys				
	290	295	300	305	
	gtc att ctg ctc cta gca ggc ttt gcc ctg ctc act ggc ctg ctc ttc				1016
	Val Ile Leu Leu Leu Ala Gly Phe Ala Leu Leu Thr Gly Leu Leu Phe				
		310	315	320	
35	atc caa atc tagggggctt caagagaggg gcaggggaga ttgatgatca ggtgc				1070

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Ile Gln Ile

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 <212> PRT
 <213> Homo sapiens

25 <400> 36

Met

1

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 30 Ala Ser Glu Pro Pro Val Pro Val Gly Leu Glu Val Lys Leu Gly Ala
 20 25 30
 Leu Val Leu Leu Leu Val Leu Thr Leu Leu Cys Ser Leu Val Pro Ile
 35 40 45
 Cys Val Leu Arg Arg Pro Gly Ala Asn His Glu Gly Ser Ala Ser Arg
 35 50 55 60 65

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Gln Lys Ala Leu Ser Leu Val Ser Cys Phe Ala Gly Gly Val Phe Leu
 70 75 80
 Ala Thr Cys Leu Leu Asp Leu Leu Pro Asp Tyr Leu Ala Ala Ile Asp
 85 90 95
 5 Glu Ala Leu Ala Ala Leu His Val Thr Leu Gln Phe Pro Leu Gln Glu
 100 105 110
 Phe Ile Leu Ala Met Gly Phe Phe Leu Val Leu Val Met Glu Gln Ile
 115 120 125
 Thr Leu Ala Tyr Lys Glu Gln Ser Gly Pro Ser Pro Leu Glu Glu Thr
 10 130 135 140 145
 Arg Ala Leu Leu Gly Thr Val Asn Gly Gly Pro Gln His Trp His Asp
 150 155 160
 Gly Pro Gly Val Pro Gln Ala Ser Gly Ala Pro Ala Thr Pro Ser Ala
 165 170 175
 15 Leu Arg Ala Cys Val Leu Val Phe Ser Leu Ala Leu His Ser Val Phe
 180 185 190
 Glu Gly Leu Ala Val Gly Leu Gln Arg Asp Arg Ala Arg Ala Met Glu
 195 200 205
 Leu Cys Leu Ala Leu Leu Leu His Lys Gly Ile Leu Ala Val Ser Leu
 20 210 215 220 225
 Ser Leu Arg Leu Leu Gln Ser His Leu Arg Ala Gln Val Val Ala Gly
 230 235 240
 Cys Gly Ile Leu Phe Ser Cys Met Thr Pro Leu Gly Ile Gly Leu Gly
 245 250 255
 25 Ala Ala Leu Ala Glu Ser Ala Gly Pro Leu His Gln Leu Ala Gln Ser
 260 265 270
 Val Leu Glu Gly Met Ala Ala Gly Thr Phe Leu Tyr Ile Thr Phe Leu
 275 280 285
 Glu Ile Leu Pro Gln Glu Leu Ala Ser Ser Glu Gln Arg Ile Leu Lys
 30 290 295 300 305
 Val Ile Leu Leu Leu Ala Gly Phe Ala Leu Leu Thr Gly Leu Leu Phe
 310 315 320
 Ile Gln Ile

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